

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lee, Jong Y.

(ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson P.C., P.A.
(B) STREET: 60 South Sixth Street, Suite 3300
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55402

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/016,159
(B) FILING DATE: 30-JAN-1998

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/876,227
(B) FILING DATE: 16-JUN-1997

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/734,097
(B) FILING DATE: 21-OCT-1996

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/460,525
(B) FILING DATE: 02-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ellinger, Mark S.
(B) REGISTRATION NUMBER: 34,812
(C) REFERENCE/DOCKET NUMBER: 07004/002004

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 612/335-5070
(B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: BamH1 linker at 5' end followed by sequence for amino acids 25 through 29 of the full length human EpoR protein. Forward primer for Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGATCC GCG CCC CCG CCT A AC
Ala Pro Pro Pro
1

23

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: EcoR1 linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human EpoR protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCTGGG GTCCAGGTCTG CT

22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)

(ix) FEATURE:

(A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Smith, D.B.
Johnson, K.S.

(B) TITLE: Single-step purification of polypeptides
expressed in Escherichia coli as fusions with
glutathione-S-transferase

(D) VOLUME: 67

(F) PAGES: 31-40

(G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GTT CCG CGT GGA T CC 18
Leu Val Pro Arg Gly
5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Winkelmann , J. C., et al.
(C) JOURNAL: Blood
(D) VOLUME: 76
(E) ISSUE: 1
(F) PAGES: 24-30
(G) DATE: 1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT 48
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15

CTC CTG CTC GCT GGG GCC GCG TGG CCC CCT AAC CTC CCG GAC 96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA 144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG 192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC 240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80

TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT 288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
85 90 95

CCC ACG GCT CGT GGT CGG GTG CGC TTC TGG TGT TCG CTG CCT ACA GCC Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala 100 105 110	336
GAC ACG TCG AGC TTC GTG CCC CTA GAG TTG CGC GTC ACA GCA GCC TCC Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser 115 120 125	384
GGC GCT CCG CGA TAT CAC CGT GTC ATC CAC ATC AAT GAA GTA GTG CTC Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu 130 135 140	432
CTA GAC GCC CCC GTG GGG CTG GTG GCG CGG TTG GCT GAC GAG AGC GGC Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly 145 150 155 160	480
CAC GTA GTG TTG CGC TGG CTC CCG CCT GAG ACA CCC ATG ACG TCT His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser 165 170 175	528
CAC ATC CGC TAC GAG GTG GAC GTC TCG GCC GGC AAC CGG CCA GGG AGC His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser 180 185 190	576
GTA CAG AGG GTG GAG ATC CTG GAG GGC CGC ACC GAG TGT GTG CTG AGC Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser 195 200 205	624
AAC CTG CGG GGC CGG ACG CGC TAC ACC TTC GCC GTC CGC GCG CGT ATG Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met 210 215 220	672
GCT GAG CCG AGC TTC GGC GGC TTC TGG AGC GCC TGG TCG GAG CCT GTG Ala Glu Pro Ser Phe Gly Phe Trp Ser Ala Trp Ser Glu Pro Val 225 230 235 240	720
TCG CTG CTG GAG CCT AGC GAC CTG GAC CCC CTC ATC CTG ACG CTC TCC Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser 245 250 255	768
CTC ATC CTC GTG GTC ATC CTG GTG CTG CTG ACC GTG CTC GCG CTG CTC Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu 260 265 270	816
TCC CAC CGC CGG GCT CTG AAG CAG AAG ATC TGG CCT GGC ATC CCG AGC Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser 275 280 285	864
CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe 290 295 300	912
CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys 305 310 315 320	960
ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu 325 330 335	1008
CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu	1056

340	345	350	
GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr 355	360	365	1104
CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp 370	375	380	1152
CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly 385	390	395	1200
TCA GAA GCA TCC TCC TGC TCA TCT GCT TTG GCC TCG AAG CCC AGC CCA Ser Glu Ala Ser Ser Cys Ser Ala Leu Ala Ser Lys Pro Ser Pro 405	410	415	1248
GAG GGA GCC TCT GCT GCC AGC TTT GAG TAC ACT ATC CTG GAC CCC AGC Glu Gly Ala Ser Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser 420	425	430	1296
TCC CAG CTC TTG CGT CCA TGG ACA CTG TGC CCT GAG CTG CCC CCT ACC Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr 435	440	445	1344
CCA CCC CAC CTA AAG TAC CTG TAC CTT GTG GTA TCT GAC TCT GGC ATC Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile 450	455	460	1392
TCA ACT GAC TAC AGC TCA GGG GAC TCC CAG GGA GCC CAA GGG GGC TTA Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu 465	470	475	1440
TCC GAT GGG CCC TAC TCC AAC CCT TAT GAG AAC AGC CTT ATC CCA GCC Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala 485	490	495	1488
GCT GAG CCT CTG CCC CCC AGC TAT GTG GCT TGC TCT TAG Ala Glu Pro Leu Pro Ser Tyr Val Ala Cys Ser 500	505		1527

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	His	Leu	Gly	Ala	Ser	Leu	Trp	Pro	Gln	Val	Gly	Ser	Leu	Cys
1			5				10						15		
Leu	Leu	Leu	Ala	Gly	Ala	Ala	Trp	Ala	Pro	Pro	Pro	Asn	Leu	Pro	Asp
			20				25					30			
Pro	Lys	Phe	Glu	Ser	Lys	Ala	Ala	Leu	Leu	Ala	Ala	Arg	Gly	Pro	Glu
					35			40				45			

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
 85 90 95

Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
 100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
 115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser
 165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser
 180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
 195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
 210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
 225 230 235 240

Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
 245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
 260 265 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
 275 280 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
 290 295 300

Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
 305 310 315 320

Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
 325 330 335

Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
 340 345 350

Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
 355 360 365

Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
 370 375 380

Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly
385 390 395 400

Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro
405 410 415

Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser
420 425 430

Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr
435 440 445

Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile
450 455 460

Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu
465 470 475 480

Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala
485 490 495

Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser
500 505